WA

PCT09

RAW SEQUENCE LISTING DATE: 10/23/2001 PATENT APPLICATION: US/09/807,660A TIME: 10:13:35

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Output Set: N:\CRF3\10232001\1807660A.raw

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3 <110> APPLICANT: Maliszewski, Charles R.
         Gayle III, Richard B.
         Marcus, Aaron J.
         Immunex Corporation
         Cornell Research Foundation, Inc.
  <120> TITLE OF INVENTION: Methods of Inhibiting Platelet Activation and
         Recruitment
12 <130> FILE REFERENCE: 23,495 PCT
14 <140> CURRENT APPLICATION NUMBER: US 09/807,660A
15 <141> CURRENT FILING DATE: 2001-04-16
17 <150> PRIOR APPLICATION NUMBER: US 60/104,585
                                                            ENTERED
18 <151> PRIOR FILING DATE: 1998-10-16
20 <150> PRIOR APPLICATION NUMBER: US 60/107,466
21 <151> PRIOR FILING DATE: 1998-11-06
23 <150> PRIOR APPLICATION NUMBER: US 60/149,010
24 <151> PRIOR FILING DATE: 1999-08-13
26 <160> NUMBER OF SEQ ID NOS: 31
28 <170> SOFTWARE: PatentIn Ver. 2.0
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33 <213> ORGANISM: Homo sapiens
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37 <222> LOCATION: (67)..(1596)
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46 aag aat atc cta gcc atc ctt ggc ttc tcc tct atc ata gct gtg ata
47 Lys Asn Ile Leu Ala Ile Leu Gly Phe Ser Ser Ile Ile Ala Val Ile
50 gct ttg ctt gct gtg ggg ttg acc cag aac aaa gca ttg cca gaa aac
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51 Ala Leu Leu Ala Val Gly Leu Thr Gln Asn Lys Ala Leu Pro Glu Asn
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54 gtt aag tat ggg att gtg ctg gat gcg ggt tct tct cac aca agt tta
55 Val Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu
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                                                                      300
58 tac atc tat aag tgg cca gca gaa aag gag aat gac aca ggc gtg gtg
59 Tyr Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val
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                                70
                                                    75
60
62 cat caa gta gaa gaa tgc agg gtt aaa ggt cct gga atc tca aaa ttt
63 His Gln Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe
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66 gtt cag aaa gta aat gaa ata ggc att tac ctg act gat tgc atg gaa
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67 Val Gln Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu
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72	,				115			,		120					125		
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76	-1-		1	130			1		135			,		140			
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		_	_	Asp		_	_	_			-		-				
80	014		145	E	9			150				5	155				
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				Asp													
84	-1-	160		110 P		Ÿ	165		9			170	0_1	U			
	aat		tat	ggc	taa	att		atc	aac	tat	cta		aac	aaa	ttc	aαt	636
		-		Gly							_	_				-	
	175		- 1 -	U 1		180				-1-	185	Lou	011	210		190	
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	-			Arg			_		-			-				_	
92	0111	L ₁ U	****	1119	195		001			200	-1-	O_Lu			205	0.2.1.	
	паа	acc	+++	gga		tta	αac	ctt	aaa		acc	tct	aca	caa		act	732
				Gly													, 52
96	OIU		1110	210	u	пси	p	шеш	215			001		220			
-	+++	αta	CCC	caa	aac	саσ	act	atc		tcc	cca	αat	aat		cta	caa	780
		_		Gln		_						-		_	-		, 00
100		, u _	225		11511	0111	1111	230		001	110	op	235		Leu	OIII	
			22.	,				200	,					,			
) +++	cac	cto	tat	aac	. aan	gac	tac	aat	ato	tac	aca	cat	age	· ++	tta	828
																ttg Leu	828
103	Phe	Arg	, Le				Asp	туг				Thr	His			ttg Leu	828
103 104	Phe	240) Leu	ı Tyr	Gly	Lys	Asp 245	Туг	Asn	Val	Tyr	Thr 250	His	Ser	Phe	e Leu	
103 104 106	Phe tgc	Arg 240 tat	J Leu J ggg	ı Tyr g aag	Gly	Lys cag	Asp 245 gca	Tyr cto	Asn tgg	Val	Tyr aaa	Thr 250	His Ggc	Ser c aag	Phe gao	e Leu	828
103 104 106 107	Phe tgc 'Cys	240 240 tat	J Leu J ggg	ı Tyr g aag	Gly	Lys cag	Asp 245 gca Ala	Tyr cto	Asn tgg	Val	Tyr aaa Lys	Thr 250 ctg	His Ggc	Ser c aag	Phe gao	e Leu c att	
103 104 106 107	Phe tgo Cys 255	240 240 tat	Gly Gly	ı Tyr g aag v Lys	Gly gat Asp	Lys cag Gln 260	Asp 245 gca Ala	t cto	tgg Trp	Val cag Gln	aaa Lys 265	Thr 250 ctg	His ggc Ala	Ser caag Lys	Phe gao Asp	e Leu c att o Ile 270	876
103 104 106 107 108	tgc Cys 255	240 240 tat Tyr	J Leu Gly Gly	ı Tyr g aag y Lys	Gly gat Asp	Lys cag Gln 260 gaa	Asp 245 gca Ala	to Tyr	tgg Trp	Val cag Gln gac	aaa Lys 265	Thr 250 ctg Leu	His gcc Ala	s Ser c aag Lys c cat	gac Asr	att o Ile 270 gga	
103 104 106 107 108 110	tgo Cys 255 cag	240 240 tat Tyr	J Leu Gly Gly	ı Tyr g aag y Lys	Gly gat Asp aat Asn	Lys cag Gln 260 gaa Glu	Asp 245 gca Ala	to Tyr	tgg Trp	Val cag Gln gac Asp	aaa Lys 265 cca	Thr 250 ctg Leu	His gcc Ala	s Ser c aag Lys c cat	gad Asr cct	e Leu c att c Ile 270 c gga c Gly	876
103 104 106 107 108 110 111	Phe tgo 'Cys 255 cag	240 240 tat Tyr gtt	g Leu ggg Gly gca Ala	aag Lys agt Ser	gat Asp aat Asn 275	Lys cag Gln 260 gaa Glu	Asp 245 gca Ala att	to Tyr	tgg Trp agg	val cag Gln gac Asp 280	aaa Lys 265 cca	Thr 250 ctg Leu tgc	His ggc Ala ttt Phe	s Ser c aag Lys c cat	gac Asp cct Pro 285	att The lead of the lead of th	876 924
103 104 106 107 108 110 111 112	Phe tgo Cys 255 cag Gln	Arg 240 tat Tyr gtt Val	y Leu ggg Gl gca Ala aag	aag Lys agt Ser	gat Asp aat Asn 275	Lys Cag Gln 260 gaa Glu	Asp 245 gca Ala att Ile	to Tyr	tgg Trp agg Arg	Val cag Gln gac Asp 280	Tyr aaa Lys 265 cca Pro	Thr 250 ctg Leu tgc Cys	His g gcc a Ala ttt phe	s Ser c aag Lys c cat e His	gac Asp cet Pro 285	e Leu c att c att c 11e 270 c gga c Gly c acc	876
103 104 106 107 108 110 113 114 115	Phe tgc Cys 255 cag Gln tat	Arg 240 tat Tyr gtt Val	y Leu ggg Gl gca Ala aag	aag Lys agt Ser gta Val	gat Asp aat Asn 275 gtg	Lys Cag Gln 260 gaa Glu	Asp 245 gca Ala att Ile	to Tyr	tgg Trp agg Arg	val cag Gln gac Asp 280 ctt	Tyr aaa Lys 265 cca Pro	Thr 250 ctg Leu tgc Cys	His g gcc a Ala ttt phe	Ser aag Lys cat His ccc	gac Asp cet Pro 285 tgc	att The lead of the lead of th	876 924
103 104 106 107 108 110 111 112 114 115	Phe tgc Cys 255 cag Gln tat	240 240 tat Tyr y y tat Val	g Let ggg Gly Gly Ala Ala g aag	aagt Lys agt Ser gta Val	gat Asp aat Asn 275 gtg Val	Lys Cag Gln 260 gaa Glu aac Asn	Asp 245 gca Ala att Ile gta Val	cto cto cto cto Leu ser	tgg Trp agg Arg Asp 295	val cag Gln gac Asp 280 ctt	aaaa Lys 265 cca Pro	Thr 250 ctg Leu tgo Cys	THIS GOOD	cate His	gac Asp cct Pro 285 tgo	e Leu c att o Ile 270 c gga o Gly o acc o Thr	876 924 972
103 104 106 107 108 110 113 114 115 116	Phe tgc Cys 255 cag Gln tat	240 240 tat Tyr y tat Val Lys	g Leu ggg Gly gca Ala aag Lys	aagy Lys agt Ser gtas Val	gat Asp aat Asn 275 gtg Val	Lys Cag Gln 260 gaa Glu aac Asn	Asp 245 gca Ala att Ile gta Val	cto Leu cto Leu ser ser	tgg Trp agg Arg Asp 295	val cag Gln gac Asp 280 ctt Leu	aaaa Lys 265 cca Pro	tgc Cys Lev tgc Cys Lys	His g gcc Ala ttt Fhe Tacc Thr	s Ser c aag Lys c cat His c ccc Pro 300 atc	gac Asp cet Pro 285 tgo Cys	e Leu c att o Ile 270 c gga o Gly o acc o Thr	876 924
103 104 106 107 108 110 111 112 114 115 116	Phe tgc Cys 255 cag Gln tat Tyr	240 240 tat Tyr y tat Val Lys	J Leu J ggg G Gl J gca Ala J aag Lys L ttt J Phe	aagy Lys agt Ser gtas Val 290 gage Glu	gat Asp aat Asn 275 gtg Val	Lys Cag Gln 260 gaa Glu aac Asn	Asp 245 gca Ala att Ile gta Val	cto Leu cto Leu ser ser	tgg Trp agg Arg Arg 295 ttc	val cag Gln gac Asp 280 ctt Leu	aaaa Lys 265 cca Pro	tgc Cys Lev tgc Cys Lys	His J gcc Ala ttt S Phe J acc Thr	s Ser aag Lys cat His ccc Pro 3000 at cat Ile	gac Asp cet Pro 285 tgo Cys	e Leu c att o Ile 270 c gga o Gly o acc o Thr	876 924 972
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103 104 106 107 108 110 113 114 115 116 118 120 122	Phe tgc Cys 255 cag Gln tat Tyr	Arg 240 tat Tyr yal Val Lys Arg	g Leu ggg Gly L gca Ala Ala g aag Lys tttt g Phe 305	aagy Lys agt Ser y gta 290 gage Glu	gat Asp aat Asn 275 gtg Val atg	Lys Cag Gln 260 gaa Glu aac Asn act	Asp 245 gca Ala att Ile gta Val ctt	ctc. Leu agt Ser cca 310 cat	tgg Trp agg Arg Asp 295 ttc	Val cag Gln gac Asp 280 ctt Leu cag Gln	aaaa Lys 265 cca Pro	tgc Cys Leu tgc Cys ttt Lys	His J gcc Ala ttt Phe J acc Thr gaa Glu 315 J gag	s Ser aag Lys cat His coc Pro 300 atc Lile	gac Asp Cet Pro 285 tgo Cys	e Leu c att o Ile 270 c gga o Gly c acc o Thr ggt o Gly	876 924 972
103 104 106 107 108 110 111 112 114 115 116 122 123	Phe tgc Cys 255 cag Gln tat Tyr aag	Arg 240 240 240 240 240 240 240 240 240 240	g Leu ggg Gly L gca Ala Ala Lys Lys Lttt Ghe 305 Asr	aagy Lys agt Ser y gta 290 gage Glu	gat Asp aat Asn 275 gtg Val atg	Lys Cag Gln 260 gaa Glu aac Asn act	Asp 245 gca Ala att Ile ytal val ctt Leu	cto Leu cto Leu ser ser cca Pro 310	tgg Trp agg Arg Asp 295 ttc	Val cag Gln gac Asp 280 ctt Leu cag Gln	aaaa Lys 265 cca Pro	tgc Cys Leu Lys Lys Lys	His J gcc J Ala L ttt S Phe J acc J Thr L gaa J gaa J Glu	s Ser aag Lys cat His coc Pro 300 atc Lile	gac Asp cet Pro 285 tgo Cys	e Leu c att o Ile 270 c gga o Gly c acc o Thr	876 924 972 1020
103 104 106 107 108 110 111 112 114 115 116 118 120 122 123 124	Phe tgc Cys 255 cag Gln tat Tyr aag Lys	Arg 240 240 240 240 240 240 240 240 240 240	g Leu ggg Gly Ala Ala y aag Lys ttt Phe 305 aac Asn	aag Lys agt Ser gta Ser 290 gag Glu tat	gat Asp aat Asn 275 gtg Val atg Met	Lys Cag Gln 260 Gaa Glu Asn Asn act Thr	Asp 245 gca Ala att Ile ytal val ctt Leu tgc Cys 325	cto Leu cto Leu ser ser cca Pro 310	tgg Trp agg Arg Asp 295 ttc	Val cag Gln gac Asp 280 ctt Leu cag Gln agc	aaaa Lys 265 cca Pro	tgc Cys Leu tgc Cys Lys ttt Phe	His G GCC Ala ttt G Phe G Thr G Glu 315 G Glu	aag Lys cat His ccc 300 atc	gac S Asp Cct Pro 285 tgo Cys Cgs	e Leu c att lie 270 c gga c Gly c acc Thr ggt Gly c acc	876 924 972 1020
103 104 106 107 108 110 111 112 114 115 116 118 120 122 123 124 126	Phe tgc Cys 255 cag Gln tat Tyr aag Lys	Arg 240 240 240 240 240 240 240 240 240 240	g Leu ggg Gly Ala aag Lys ttt Phe 305 aac Asn	aag Lys agt Ser ygta Ser 290 gag Glu tat tyr	gat Asp aat Asn 275 gtg Val atg Met	Lys Cag Gln 260 Gaa Glu Asn act Thr	Asp 245 gca Ala att Ile ytal val ctt Cys 325 tcc	cto Leu cto Leu ser ser cca 310 cat His	tgg Trp agg Arg Asp 295 ttc Phe	Val cag Gln gac Asp 280 ctt Leu cag Gln agc Ser	aaaa Lys 265 cca Pro	tgo Cys Leu tgo Cys Lys ttt Phe	His Grant Ala Crant	aag Lys cat His ccc 300 atc	gac Asp Cet Pro 285 tgo Cys Cgs	e Leu c att c Ile 270 c gga c Gly d acc s Thr ggt ggt gdy c acc s Asn	876 924 972 1020
103 104 106 107 108 110 111 112 114 115 116 118 112 123 124 126 127	tgc Cys 255 cag Gln tat Tyr aag Lys	Arg 240 tat Tyr gtt Val aag Lys aga Arg 320 agt Ser	g Leu ggg Gly Ala aag Lys ttt Phe 305 aac Asn	aag Lys agt Ser ygta Ser 290 gag Glu tat tyr	gat Asp aat Asn 275 gtg Val atg Met	Lys Cag Gln 260 gaa Glu Asn act Thr	Asp 245 gca Ala att Ile gta Val ctt Leu tgc Cys 325 tcc Ser	cto Leu cto Leu ser ser cca pro 310 cat His	tgg Trp agg Arg Asp 295 ttc Phe	Val cag Gln gac Asp 280 ctt Leu cag Gln agc Ser	tace Tyr cag Gln atce The	tgc Cys Leu tgc Cys Lys ttt Phe Leu 330 aat	His Grant Ala Crant	aag Lys cat His ccc 300 atc	gac Asp Cet Pro 285 tgo Cys Cgs	e Leu c att c Ile 270 c gga c Gly d acc Thr ggt d Gly c aac c Asn c ttg	876 924 972 1020
103 104 106 107 108 110 111 112 114 115 116 112 123 124 126 127 128	tgc Cys 255 cag Gln tat Tyr aag Lys	Arg 240 tat Tyr gtt Val aag Lys aga Arg 320 agt Ser	g Leu g g g g G l y a a g L y s t t t t g Phe 305 a a c As n	aagt Lys agt Ser y gta Ser y gta 290 gag gag tat Tyr tgc	gat Asp aat Asn 275 gtg Val atg Met caa Gln	Lys cag Gln 260 gaa Glu aac Asn act Thr	Asp 245 gca Ala att Ile gta Val ctt Leu tgc Cys 325 tcc	cto Leu cto Leu agt Ser cca Pro 310 cat His	tgg Trp agg Arg Asp 295 ttc Phe	val cag Gln gac Asp 280 ctt Leu cag Gln agc Ser	tace Tyr cag Gln atce The 345	tgc Cys Leu tgc Cys Lys ttt Phe ctg Lau 330 aat	His J gcc J gcc J Ala C ttt S Phe J acc S Thr J gag J gag J ggg	aaga Lys cat His CCC 300 atc Ile Ctc Leu att	gac Asp cct Pro 285 ctg Cys cac Glr tto	e Leu c att lie 270 c gga o Gly c acc Thr ggt o Gly c acc t tug c Leu 350	876 924 972 1020 1068 1116
103 104 106 107 108 110 111 112 114 115 116 112 123 124 126 127 128 130	tgc Cys 255 cag Gln tat Tyr aag Lys att	Arg 240 tat Tyr gtt Val aag Arg 320 agt Ser	g Leu g g g g G l y Ala g aag Lys ttt phe 305 aag Asn tag tag tag	aagt Lys agt agt Ser y gta Ser y gta 290 gag gag gag tat Tyr c tgc cag	gat Asp aat Asn 275 gtg Val atg Met caa Gln cct pro	Lys cag Gln 260 gaa Glu aac Asn act Thr caa Gln tac Tyr 340	Asp 245 gca Ala att Ile gta Val ctt Leu tgc Cys 325 tcc Ser	ctc Leu ctc Leu agt Ser cca 310 cat His	tgg Trp agg Arg Asp 295 ttc Phe caa Gln	val cag Gln gac Asp 280 ctt Leu cag Gln agc Ser	tace Tyr cag Gln atce The 345 tca	tgc Cys Leu tgc Cys Lys ttt Phe ctg Lau 330 aat Asn	His J gcc J gcc J Ala C ttt S Phe J acc S Thr J gag J gag J ggg J Glu	aaga Lys cat His CCC 300 atc Ile Inter Ile	gac Asp cct Pro 285 ctgo Cys cac Glr tto Phe	e Leu c att le 270 c gga c Gly c acc Thr ggt d Gly c acc t Leu 350 c gtg	876 924 972 1020
103 104 106 107 108 110 111 112 114 115 116 112 123 124 126 127 128 130	tgc Cys 255 cag Gln tat Tyr aag Lys att Thr 335 cca	Arg 240 tat Tyr gtt Val aag Arg 320 agt Ser	g Leu g g g g G l y Ala g aag Lys ttt phe 305 aag Asn tag tag tag	aagt Lys agt agt Ser y gta Ser y gta 290 gag gag gag tat Tyr c tgc cag	gat Asp aat Asn 275 gtg Val atg Met caa Gln cct pro	Lys Cag Gln 260 gaa Glu aac Asn act Thr Caa Gln tac Tyr 340 gat	Asp 245 gca Ala att Ile gta Val ctt Leu tgc Cys 325 tcc Ser	ctc Leu ctc Leu agt Ser cca 310 cat His	tgg Trp agg Arg Asp 295 ttc Phe caa Gln	val cag Gln gac Asp 280 ctt Leu cag Gln agc Ser	tace Tyr cag Gln atce The 345 tca Ser	tgc Cys Leu tgc Cys Lys ttt Phe ctg Lau 330 aat Asn	His J gcc J gcc J Ala C ttt S Phe J acc S Thr J gag J gag J ggg J Glu	aaga Lys cat His CCC 300 atc Ile Inter Ile	gac Asp cct Pro 285 ctgo Cys cac Glr tto Phe	e Leu c att le 270 c gga c Gly c acc Thr d Gly c aac k Asn c ttg c Leu 350 c gtg val	876 924 972 1020 1068 1116

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143	Thr		Tyr	Ala	Gly	Val	_	Glu	Lys	Tyr	Leu		Glu	Tyr	Cys	Phe	
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										-					ttc		1356
		Gly	Thr	Tyr	Ile		Ser	Leu	Leu	Leu		GLY	Tyr	His	Phe		
	415					420					425					430	
	_	-										_			ggc		1404
	Ala	Asp	Ser	Trp		His	Ile	His	Phe		GLY	Lys	Ile	GIn	Gly	Ser	
152				_	435					440					445		1.50
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	Pro	Ala		GIn	Pro	Leu	Ser		Pro	Leu	Ser	HIS		Thr	Tyr	vaı	
160			465					470					475				1540
			_	_				_	-					-	atc		1548
	Pne		мет	vaı	Leu	Pne		Leu	vaı	Leu	Pne		vaı	Ата	Ile	ire	
164		480	- 4- 4-				485					490					1506
		_					_							-	atg	_	1596
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180	1	Giu	тэр	1111	Бу 5 5	,	JCI	ASII	VUL	10	1111	1110	Cy5	DCI	15	21511	
		T.011	Δla	Tle	_	Glv	Phe	Ser	Ser		Tle	Δla	Va 1	Tle	Ala	Leu	
183	110	DCu	niu	20	пси	011	1110	DCI	25	110	***	****	, u i	30		Deu	
	Len	Δla	Val		Leu	Thr	Gln	Agn		Δla	Len	Pro	Glu		Val	Lvs	
186	шец	inta	35	017	neu	* ***	0111	40	2,5		LCu		45		, 41	_15	
	Tvr	G1 v		Va l	Leu	Asp	Ala		Ser	Ser	His	Thr		Leu	Tyr	Tle	
189	- 1 -	50	110		Lea		55	011	001	001	113.0	60	00.		- 1 -		
	Tur		Tro	Pro	Ala	Glu		.Glu	Asn	Asp	Thr		Va l	Va l	His	Gln	
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195				J_ J	85		-10	1		90			-10		95		
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201	- ,		115			,		120					125		-		

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203 204	Gly	Ala 130	Thr	Ala	Gly	Met	Arg 135	Leu	Leu	Arg	Met	Glu 140	Ser	Glu	Glu	Leu
	λ 1 ¬		7 ~~	Wa I	TOU	7 an		175 T	C1u	λνα	Sor		Ser	λen	Птит	Dro
		кър	AIG	Val	ьец		Val	Val	GLu	Arg		пеп	Ser	N3II	1 Y 1	160
	145	_	-1	~ 1	~ 3	150	_		~ 7	1	155	~1 .	a 1	a 1	01	
	Phe	Asp	Phe	Gin	_	Ата	Arg	тте	шe		GTĀ	GIn	Glu	Glu		АТа
210					165					170					175	
212	Tyr	Gly	Trp	Ile	Thr	Ile	Asn	Tyr	Leu	Leu	Gly	Lys	Phe	Ser	Gln	Lys
213				180					185					190		
215	Thr	Arq	Trp	Phe	Ser	Ile	Val	Pro	Tyr	Glu	Thr	Asn	Asn	Gln	Glu	Thr
216		_	195					200	-				205	•		
	Phe	Glv	Δla	Len	Asp	Len	Glv	Glv	Ala	Ser	Thr	Gln	Val	Thr	Phe	Val
219	1110	210		LCu.			215			001		220	,		2	,
	D							Com	Dwo	7.00	7		T 011	C1 n	Dho	7 ma
		GIII	ASII	GIII	1111		GIU	ser	PIO	ASP		Ата	Leu	GIII	Pile	
	225	_		_	_	230	_		_	_,	235	_	_,	_	_	240
	Leu	Tyr	GTA	Lys		Tyr	Asn	Val	Tyr		His	Ser	Phe	Leu		Tyr
225					245					250					255	
227	Gly	Lys	Asp	Gln	Ala	Leu	Trp	Gln	Lys	Leu	Ala	Lys	Asp	Ile	Gln	Val
228				260					265					270		
230	Ala	Ser	Asn	Glu	Ile	Leu	Arg	Asp	Pro	Cys	Phe	His	Pro	Gly	Tyr	Lys
231			275				_	280		-			285	-	-	-
	Lvs	Va l		Asn	Val	Ser	Asp		Tvr	Lvs	Thr	Pro	Cys	Thr	Lvs	Ara
234	L , 5	290	,	11011	• • •	UCI	295	Deu	-1-	1 10	* ***	300	0 10			
	Dho		Wot	mb ~	T OU	Dro	_	Cln	Cln	Dho	C1		Gln	C117	т10	C111
		GIU	Met	1117	rea		Pne	GIII	GIII	Pne		TTE	GIII	GIY	TIE	
237	305	_			_	310		_		_	315	_	-1	_		320
	Asn	Tyr	GIn	GIn	_	His	GIn	Ser	IIe		GLu	Leu	Phe	Asn		Ser
240					325					330					335	
242	Tyr	Cys	Pro	Tyr	Ser	Gln	Cys	Ala		Asn	Gly	Ile	Phe	Leu	Pro	Pro
243				340					345					350		
245	Leu	Gln	Gly	Asp	Phe	Gly	Ala	Phe	Ser	Ala	Phe	Tyr	Phe	Val	Met	Lys
246			355	_				360					365			
248	Phe	Leu	Asn	Leu	Thr	Ser	Glu	Lvs	Val	Ser	Gln	Glu	Lys	Val	Thr	Glu
249		370					375	-1-				380	1 -			
_	Mot		Luc	T.vc	Dho	Cve		Gln	Dro	Trn	Glu		Ile	T.vc	Thr	Ser
	385	Mec	пуз	цуз	riic	390	AIU	0111	110	111	395	Olu	110	цуз	1111	400
		×1 -	C1	37- 1	T		T	Л	T 0	Com		m	Crra	Dha	C 0 m	
	TYL	AIA	СТА	val	_	GIU	ьуѕ	TAL	Leu		GIU	TAT	Cys	PHE		GIY
255		_		_	405	_	_	_		410	_	•			415	_
	Thr	Tyr	IIe		Ser	Leu	Leu	Leu		GTA	Tyr	HIS	Phe		Ala	Asp
258				420					425					430		
260	Ser	${\tt Trp}$	Glu	His	Ile	His	Phe	Ile	Gly	Lys	Ile	Gln	Gly	Ser	Asp	Ala
261			435					440					445			
263	Gly	Trp	Thr	Leu	Gly	Tyr	Met	Leu	Asn	Leu	Thr	Asn	Met	Ile	Pro	Ala
264	-	450			_	-	455					460				
	G111		Pro	Len	Ser	Thr	Pro	Leu	Ser	His	Ser	Thr	Tyr	Val	Phe	Leu
267						470					475		-1-			480
		Val	LOU	Dho	Cor		Wa 1	LOU	Dho	Thr		λΊэ	·Ile	Tlo	G1 v	
	MEL	Val	пец	FIIE	485	пец	val	neu	r 11G		v u.⊥	лта	TTE	116		Leu
270	T	T 1 -	DL -	TT.1 =		D-:-	a	т	nl	490	T	7	We ±	17- 7	495	
	ьeu	тте	rne		гĀ2	Pro	ser	ryr		Trp	ьys	Asp	Met			
273	_			500					505					510		
276	<210)> SE	EQ II	ON C	3											

RAW SEQUENCE LISTING DATE: 10/23/2001 PATENT APPLICATION: US/09/807,660A TIME: 10:13:35

Input Set: A:\09-807660 Sequence Listing.txt
Output Set: N:\CRF3\10232001\1807660A.raw

```
277 <211> LENGTH: 476
278 <212> TYPE: PRT
279 <213> ORGANISM: Artificial Sequence
281 <220> FEATURE:
·282 <223> OTHER INFORMATION: Description of Artificial Sequence: Fusion
          construct of human CD39
285 <400> SEQUENCE: 3
286 Met Ala Thr Ser Trp Gly Thr Val Phe Phe Met Leu Val Val Ser Cys
287
289 Val Cys Ser Ala Val Ser His Arg Asn Gln Gln Thr Trp Phe Glu Gly
290
                                      25
                 20
292 Ile Phe Leu Ser Ser Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys
295 Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile
296
298 Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His Gln
299
301 Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln
                     85
                                          90
304 Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala
                                     105
307 Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu
308
            115
                                 120
310 Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu
                             135
                                                 140
311
        130
313 Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro
                         150
                                             155
316 Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Gly Ala
                    165
                                         170
319 Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys
320
322 Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr
323
            195
                                 200
325 Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr Phe Val
                             215
                                                 220
328 Pro Gln Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg
329 225
                         230
                                             235
331 Leu Tyr Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr
332
                    245
                                         250
334 Gly Lys Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val
335
                260
                                     265
                                                          270
337 Ala Ser Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys
            275
                                 280
340 Lys Val Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg
341
                             295
343 Phe Glu Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly
344 305
                                             315
                         310
346 Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser
347
                    325
                                         330
```

Use of n and / or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to ensure a corresponding explanation is present in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY

DATE: 10/23/2001

PATENT APPLICATION: US/09/807,660A

TIME: 10:13:36

Input Set : A:\09-807660 Sequence Listing.txt
Output Set: N:\CRF3\10232001\1807660A.raw

L:398 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4